

FIG. 1

FIG. 2-A

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1/1	31/11
CAA AAC TTC CTA ATT TCT CAA TGT ATT ACT	AAT TAA TAG AAA GTT TGT TTT ATT TTC ATG
gln asn phe leu ile ser gln cys ile thr	asn OCH AMB lys val cys phe ile phe met
61/21	91/31
TGG ATA AAT GAA TTA TTT TCT CTA TAC CGG	CAT TTG CAT GCA ATT TTG TAT GAC TAA AAT
trp ile asn glu leu phe ser leu tyr arg	his leu his ala ile leu tyr asp OCH asn
121/41	151/51
GTA AAT AAT TAT TTG CAT GCA ATT ATG TGG	GCA TGT CAT AGT TTT TCA AGA ATA ATA ATA
val asn asn tyr leu his ala ile met trp	ala cys his ser phe ser arg ile ile ile
181/61	211/71
AGA TGA CAT GAC AAG ATA TTC AAA AAA ATT	TGA TGA TTA TAT GTT GAA GTT AAT TGA ACT
arg OPA his asp lys ile phe lys lys ile	OPA OPA leu tyr val glu val asn OPA thr
241/81	271/91
AAA AAG TAA TTA AGT AAA ATG GAC ATA GGA	AAC AAC GTG GAA GAA CAT CAG GAA TAT ATT
lys lys OCH leu ser lys met asp ile gly	asn asn val glu glu his gln glu tyr ile
301/101	331/111
TCT GGA CCA TAC ATT GCA TTA ATT AAT GGC	ACT AAT CAA CAA AGG GAA CCG AAT AAA AAG
ser gly pro tyr ile ala leu ile asn gly	thr asn gln gln arg glu pro asn lys lys
361/121	391/131
TTG AAA AAC ATA ATA ATT GCA ACG TTG ATT	GCA ATC TTT ATA GTT TTG GTT GTT ACT GTA
leu lys asn ile ile ile ala thr leu ile	ala ile phe ile val leu val val thr val
421/141	451/151
TCT TTG TAT ATT ACT AAT AAC ACC AGT GAC	AAA ATT GAC GAT TTC GTA CCT GGT GAT TAT
ser leu tyr ile thr asn asn thr ser asp	lys ile asp asp phe val pro gly asp tyr
481/161	511/171
GTT GAT CCA GCA ACT AGG GAG TAT AGA AAG	AGT TTT GAG GAG TTC AAA AAG AAA TAC CAC
val asp pro ala thr arg glu tyr arg lys	ser phe glu glu phe lys lys lys tyr his
541/181	571/191
AAA GTA TAT AGC TCT ATG GAG GAG GAA AAT	CAA AGA TTT GAA ATT TAT AAG CAA AAT ATG
lys val tyr ser ser met glu glu glu asn	gln arg phe glu ile tyr lys gln asn met
601/201	631/211
AAC TTT ATT AAA ACA ACA AAT AGC CAA GGA	TTC AGT TAT GTG TTA GAA ATG AAT GAA TTT
asn phe ile lys thr thr asn ser gln gly	phe ser tyr val leu glu met asn glu phe
661/221	691/231
GGT GAT TTG TCG AAA GAA GAG TTT ATG GCA	AGA TTC ACA GGA TAT ATA AAA GAT TCC AAA
gly asp leu ser lys glu glu phe met ala	arg phe thr gly tyr ile lys asp ser lys
721/241	751/251
GAT GAT GAA AGG GTA TTT AAG TCA AGT AGA	GTC TCA GCA AGC GAA TCA GAA GAG GAA TTT
asp asp glu arg val phe lys ser ser arg	val ser ala ser glu ser glu glu glu phe
781/261	811/271
GTT CCC CCA AAT TCT ATT AAT TGG GTG GAA	GCT GGA TGC GTG AAC CCA ATA AGA AAT CAA
val pro pro asn ser ile asn trp val glu	ala gly cys val asn pro ile arg asn gln
841/281	871/291
AAG AAT TGT GGG TCA TGT TGG GCT TTC TCT	GCT GTT GCA GCT TTG GAG GGA GCA ACG TGT
lys asn cys gly ser cys trp ala phe ser	ala val ala ala leu glu gly ala thr cys
901/301	931/311
GCT CAA ACA AAC CGA GGA TTA CCA AGC TTG	AGT GAA CAG CAA TTT GTT GAT TGC AGT AAA
ala gln thr asn arg gly leu pro ser leu	ser glu gln gln phe val asp cys ser lys

FIG. 2-B

961/321

CAA AAT GGC AAC TTT GGA TGT GAT GGA GGA ACA ATG GGA TTG GCT TTT CAG TAT GCA ATT
gln asn gly asn phe gly cys asp gly gly thr met gly leu ala phe gln tyr ala ile
1021/341

AAG AAC AAA TAT TTA TGT ACT AAT GAT GAT TAC CCT TAC TTT GCT GAG GAA AAA ACA TGT
lys asn lys tyr leu cys thr asn asp asp tyr pro tyr phe ala glu glu lys thr cys
1081/361

ATG GAT TCA TTT TGC GAG AAT TAT ATA GAG ATT CCT GTA AAA GCC TAC AAA TAT GTA TTT
met asp ser phe cys glu asn tyr ile glu ile pro val lys ala tyr lys tyr val phe
1141/381

CCG AGA AAT ATT AAT GCA TTA AAG ACT GCT TTG GCT AAG TAT GGA CCA ATT TCA GTT GCA
pro arg asn ile asn ala leu lys thr ala leu ala lys tyr gly pro ile ser val ala
1201/401

ATT CAG GCC GAT CAA ACC CCT TTC CAG TTT TAT AAA AGT GGA GTA TTC GAT GCT CCT TGT
ile gln ala asp gln thr pro phe gln phe tyr lys ser gly val phe asp ala pro cys
1261/421

GGA ACC AAG GTT AAT CAT GGA GTT GTT CTA GTT GAA TAT GAT ATG GAT GAA GAT ACT AAT
gly thr lys val asn his gly val val leu val glu tyr asp met asp glu asp thr asn
1321/441

AAA GAA TAT TGG CTA GTA AGA AAT AGC TGG GGT GAA GCG TGG GGA GAG AAA GGA TAC ATC
lys glu tyr trp leu val arg asn ser trp gly glu ala trp gly glu lys gly tyr ile
1381/461

AAA CTA GCT CTT CAT TCT GGA AAG AAG GGA ACA TGT GGT ATA TTG GTT GAG CCA GTG TAT
lys leu ala leu his ser gly lys lys gly thr cys gly ile leu val glu pro val tyr
1441/481

CCA GTG AAT AAT CAA TCA ATA TAA GCA TTT CAG TGT TTG ACT AAG TAA TTC TAA TAT ATT
pro val ile asn gln ser ile OCH ala phe gln cys leu thr lys OCH phe OCH tyr ile
1501/501

TCA GCA TTC TCA GAG ATA ATT TTA GTT CAA ATG AAC AAT CTA TTC ATA TAT ATA AGC ATT
ser ala phe ser glu ile ile leu val gln met asn asn leu phe ile tyr ile ser ile
1561/521

CCA TAC TTA ATT ATT TAT TGA TTT TAA TAA AAT GTT TGG CTA AAG AAA GCA ATC AAG ATA
pro tyr leu ile ile tyr OPA phe OCH OCH asn val trp leu lys lys ala ile lys ile
1621/541

ATT TAT GGA CGT TCT ATT GTT CTT ACT TCA ATA ATA ATC CTT
ile tyr gly arg ser ile val leu thr ser ile ile ile leu

991/331

1051/351

1111/371

1171/391

1231/411

1291/431

1351/451

1411/471

1471/491

1531/511

1591/531

1651/551

FIG. 3-A

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met	asp	ile	gly	asn	asn	val	glu	glu	his	gln	glu	tyr	ile	ser	1	5	10	15
gly	pro	tyr	ile	ala	leu	ile	asn	gly	thr	asn	gln	gln	arg	glu	20	25	30	
pro	asn	lys	lys	leu	lys	asn	ile	ile	ile	ala	thr	leu	ile	ala	35	40	45	
ile	phe	ile	val	leu	val	val	thr	val	ser	leu	tyr	ile	thr	asn	50	55	60	
asn	thr	ser	asp	lys	ile	asp	asp	phe	val	pro	gly	asp	tyr	val	65	70	75	
asp	pro	ala	thr	arg	glu	tyr	arg	lys	ser	phe	glu	glu	phe	lys	80	85	90	
lys	lys	tyr	his	lys	val	tyr	ser	ser	met	glu	glu	glu	asn	gln	95	100	105	
arg	phe	glu	ile	tyr	lys	gln	asn	met	asn	phe	ile	lys	thr	thr	110	115	120	
asn	ser	gln	gly	phe	ser	tyr	val	leu	glu	met	asn	glu	phe	gly	125	130	135	
asp	leu	ser	lys	glu	glu	phe	met	ala	arg	phe	thr	gly	tyr	ile	140	145	150	
lys	asp	ser	lys	asp	asp	glu	arg	val	phe	lys	ser	ser	arg	val	155	160	165	
ser	ala	ser	glu	ser	glu	glu	glu	phe	val	pro	pro	asn	ser	ile	170	175	180	
asn	trp	val	glu	ala	gly	cys	val	asn	pro	ile	arg	asn	gln	lys	185	190	195	
asn	cys	gly	ser	cys	trp	ala	phe	ser	ala	val	ala	ala	leu	glu	200	205	210	
gly	ala	thr	cys	ala	gln	thr	asn	arg	gly	leu	pro	ser	leu	ser	215	220	225	
glu	gln	gln	phe	val	asp	cys	ser	lys	gln	asn	gly	asn	phe	gly	230	235	240	
cys	asp	gly	gly	thr	met	gly	leu	ala	phe	gln	tyr	ala	ile	lys	245	250	255	
asn	lys	tyr	leu	cys	thr	asn	asp	asp	tyr	pro	tyr	phe	ala	glu	260	265	270	
glu	lys	thr	cys	met	asp	ser	phe	cys	glu	asn	tyr	ile	glu	ile	275	280	285	
pro	val	lys	ala	tyr	lys	tyr	val	phe	pro	arg	asn	ile	asn	ala	290	295	300	
leu	lys	thr	ala	leu	ala	lys	tyr	gly	pro	ile	ser	val	ala	ile	305	310	315	
gln	ala	asp	gln	thr	pro	phe	gln	phe	tyr	lys	ser	gly	val	phe	320	325	330	
asp	ala	pro	cys	gly	thr	lys	val	asn	his	gly	val	val	leu	val				

FIG. 3-B

335	340	345
glu tyr asp met	asp glu asp thr asn lys glu tyr trp leu val	
350	355	360
arg asn ser trp	gly glu ala trp gly glu lys gly tyr ile lys	
365	370	375
leu ala leu his	ser gly lys lys gly thr cys gly ile leu val	
380	385	390
glu pro val tyr	pro val ile asn gln ser ile	
395	400 403	SEQ ID NO: 4

FIG. 4

60
 PapainMAM IPSISKLLFV AICLFVYMG
 Cryptopain MDIGNNVEEH QEYISGPYIA LINGTNQORE PNKKLNIII ATLIAFIVL VVTVSLYITN
 P.v., mature
 130
 SFGFSI.VG YSQNDLTSTE RLIQLFESWM LKHNKIYKNI DEKIYRFEIF KDNLYIDET NKKNNSYWL
 NTSKIDDFV PGDYVDPATR EYRKSFEFK KKYHKVYSSM EENQRFEIY KQNMFIKT NSQGFSYVLE

 200
 LNVFADMSND EFKEKYTGSI AGNY....TT TELSYYEVLN DGDVNIPEYV DWRQKGAVTP VKNQSGCGSC
 MNEFGDLSKE EFMARFTGYI KDSKDDERVF KSSRVSASES EEEFVPPNSI NWVEAGCVNP IRNQKNCGSC
FPDSR DYRSKFNFLP PKDQGNCGSC
 CGSC
 270
 WAFSAVVTIE GIIKIRTG.N LNEYSEQELL DCDR..RSYG CNGGYPWSAL QLVAQY.GIH YRNTYPYEGV
 WAFSAVAALE GATCAQNRG LPSLSEQQFV DCSKQNGNFG CDGGTMGLAF QYAIKNKYLC TNDYYPYFAE
 WAFAAIGNFE YLYVHTRHEM PISFSEQQMV DCST..ENYV CDGGNPFYAF LYMINN.GVC LGDEYPYKGH
 WAF
 340
 QRYC.RSREK GPYAAKTDGV RQVQPYNEGA LLYSIAN..Q PVSVVLEAAG KDFQLYRGGI FVGPCGNKVD
 EKTCDMSFCE NYIEIPYKAY KYVFPRNINA LKTALAKY.G PISVAIQADQ TPFQFYKSGV FDAPCGTKVN
 EDFFCLNYRC SLLGRVHFIG DVKPNELIMA L.....NYVG PVTIAVGA.S EDFVLYSGGV FDGECNPELN
 410
 HAVAAVGYGPNYILI KNSWGTGWG ENGYIRIKRG
 HGVVLVGYDM DEDTNKE...YWL V RNSWGEAWG EKGYIKLALH
 HSVLLVGYGQ VKKSLAFEDS HSNVDSNLK KYKENIKGDD DDDIYYWIV RNSWGNPWG EGGYIRIKRN
 YWL V RNSW
 433
 TGNSYGVCGL YTSSFVPVK N ... SEQ ID NO: 7
 .SGKKGTGGI LVEPVVPV N QSI
 KAGDDGFCGV GSDVFFPIY. ... SEQ ID NO: 8

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FIG. 5

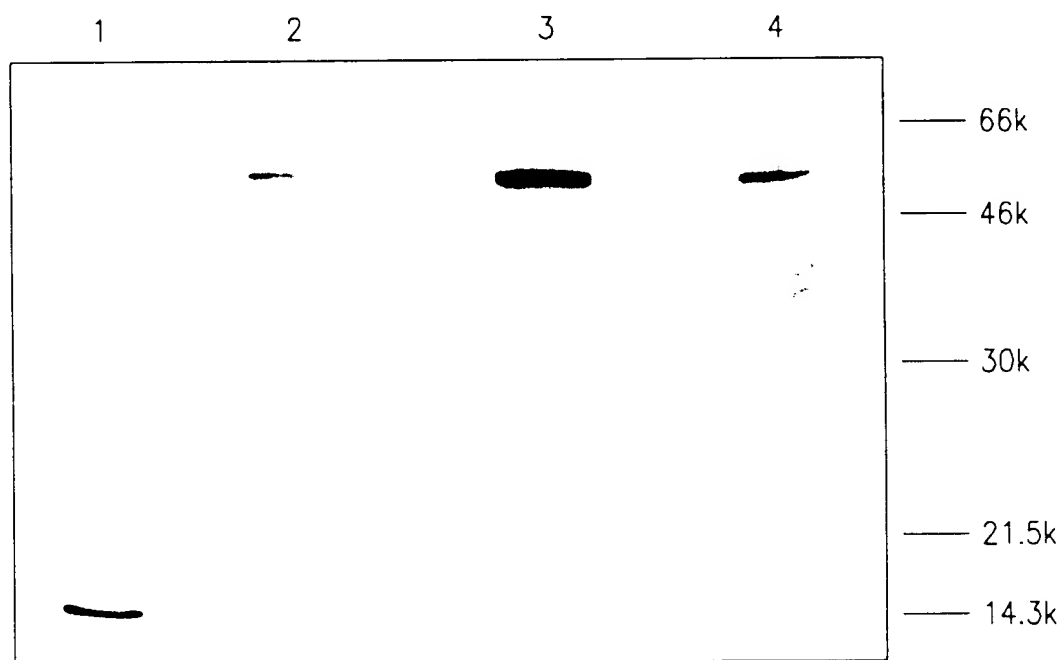
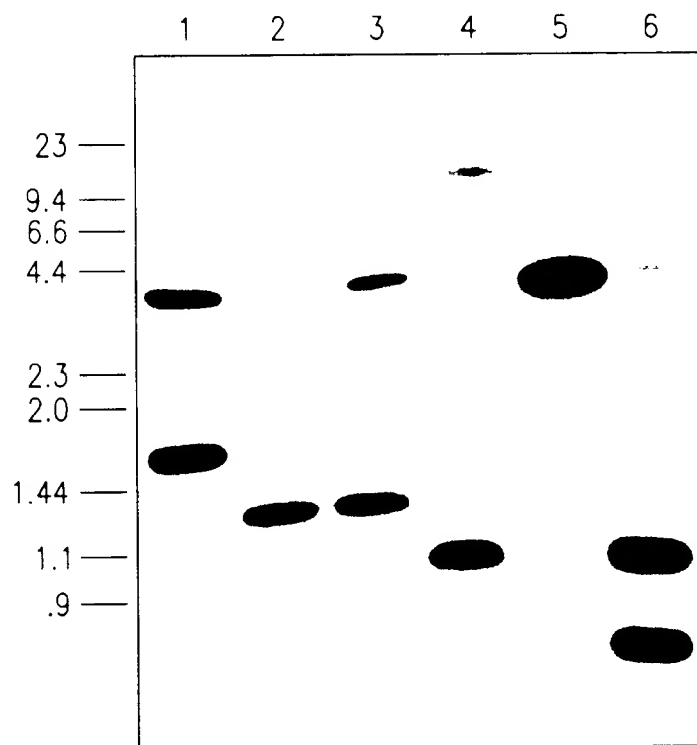


FIG. 6

FIG. 6

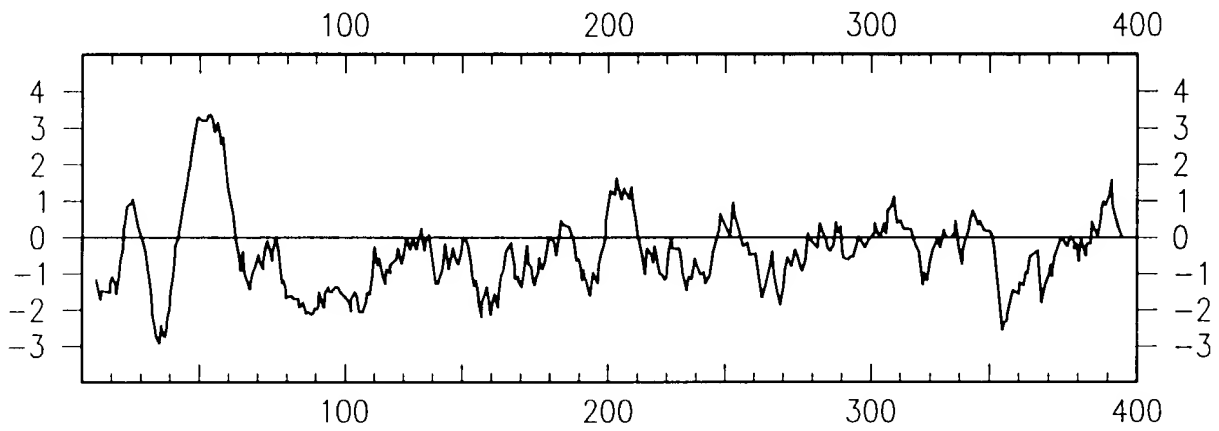


FIG. 7A

1. AAAGGATCCT GC/TGGIA/TG/CITG C/TTGGGCITT
2. TTTGAATTCC CAIG/CA/TA/GTTIC/T T/GIAC/TIATCCA A/GTA

1. CCAGGTACCA TGGACATAGG AAAC
2. CCCTCTAGAT GCTTATATTG ATTG

FIG. 7B

FIG. 8

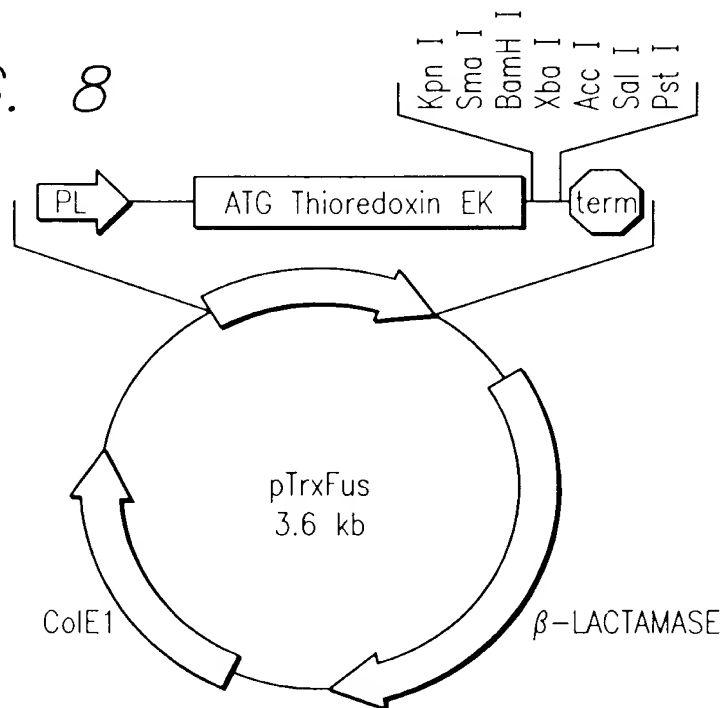


FIG. 10A

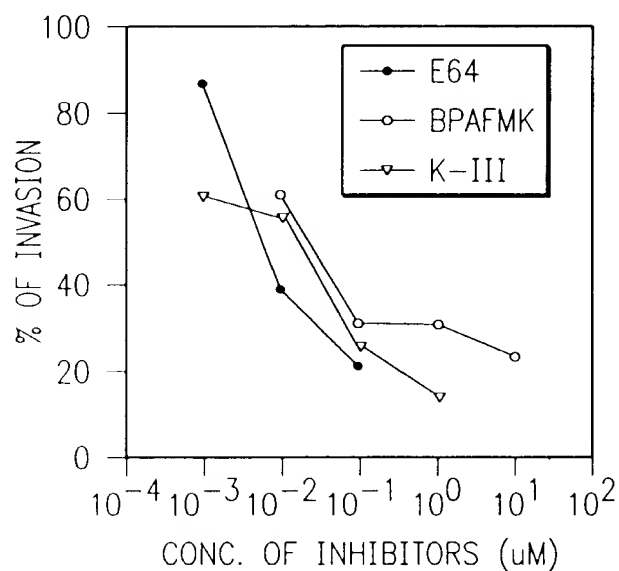


FIG. 10B

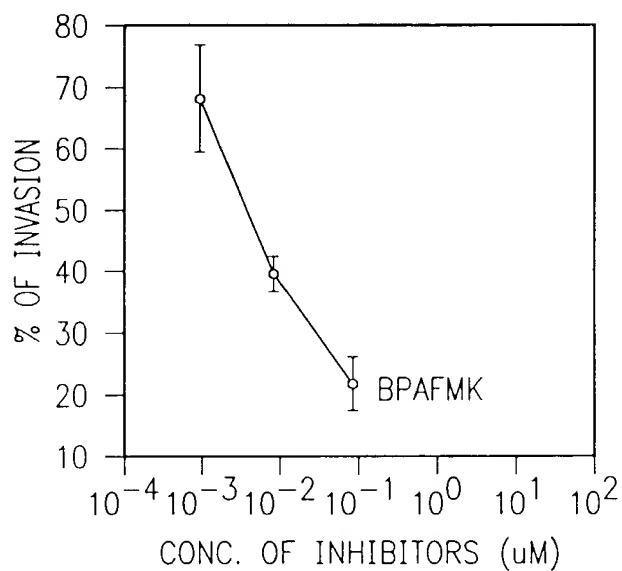


FIG. 10C

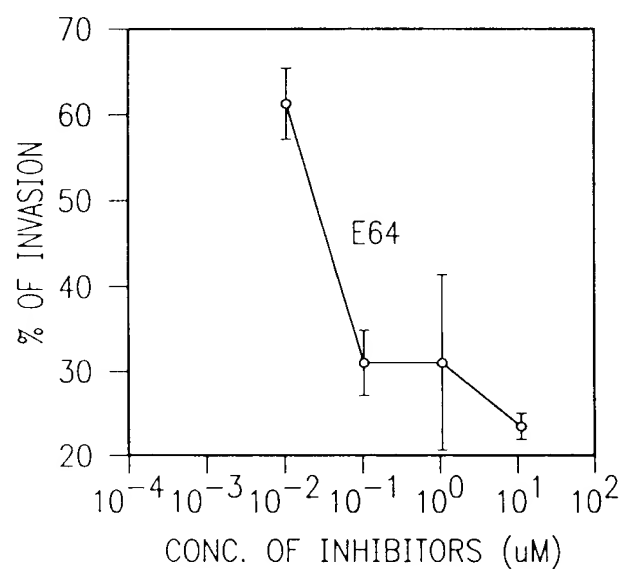


FIG. 10D

